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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/509,796

DATE: 10/08/2004  
TIME: 12:01:03

Input Set : A:\PTO.FG.txt  
Output Set: N:\CRF4\10082004\J509796.raw

5 <110> APPLICANT: BASF Plant Science GmbH  
7 <120> TITLE OF INVENTION: Expression of Phospholipids:Diacylglycerine Acyltransferase (PDAT) for  
8 the Production of Plant Storage Lipids with Polyunsaturated Fatty Acids  
W--> 9 <130> FILE REFERENCE: 1  
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/509,796  
C--> 10 <141> CURRENT FILING DATE: 2004-09-29  
W--> 10 <160> NUMBER OF SEQ ID: 2  
11 <170> SOFTWARE: PatentIn version 3.1  
W--> 12 <210> SEQ ID NO: 1  
13 <211> LENGTH: 2425  
14 <212> TYPE: DNA  
15 <213> ORGANISM: Physcomitrella patens  
17 <220> FEATURE:  
19 <221> NAME/KEY: CDS  
21 <222> LOCATION: (120)..(2135)  
23 <223> OTHER INFORMATION: Phospholipid:Diacylglycerin-Acyltransferase  
26 <400> SEQUENCE: 1  
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29 ctggacgaga ttgacaaag tccgtatagc ttaacctggt ttaatttcaa gtgacagat 119  
31 atg ccc ctt att cat cgg aaa aag ccg acg gag aaa cca tcg acg ccg 167  
32 Met Pro Leu Ile His Arg Lys Lys Pro Thr Glu Lys Pro Ser Thr Pro  
33 1 5 10 15  
35 cca tct gaa gag gtg gtg cac gat gag gat tcg caa aag aaa cca cac 215  
36 Pro Ser Glu Glu Val Val His Asp Glu Asp Ser Gln Lys Lys Pro His  
37 20 25 30  
39 gaa tct tcc aaa tcc cac cat aag aaa tcg aac gga gga ggg aag tgg 263  
40 Glu Ser Ser Lys Ser His His Lys Lys Ser Asn Gly Gly Gly Lys Trp  
41 35 40 45  
43 tcg tgc atc gat tct tgt tgt tgg ttc att ggg tgt gtg tgt gta acc 311  
44 Ser Cys Ile Asp Ser Cys Cys Trp Phe Ile Gly Cys Val Cys Val Thr  
45 50 55 60  
47 tgg tgg ttt ctt ctc ttc ctt tac aac gca atg cct gcg agc ttc cct 359  
48 Trp Trp Phe Leu Leu Phe Leu Tyr Asn Ala Met Pro Ala Ser Phe Pro  
49 65 70 75 80  
51 cag tat gta acg gag cga atc acg ggt cct ttg cct gac ccg ccc ggt 407  
52 Gln Tyr Val Thr Glu Arg Ile Thr Gly Pro Leu Pro Asp Pro Pro Gly  
53 85 90 95  
55 gtt aag ctc aaa aaa gaa ggt ctt aag gcg aaa cat cct gtt gtc ttc 455  
56 Val Lys Leu Lys Lys Glu Gly Leu Lys Ala Lys His Pro Val Val Phe  
57 100 105 110  
59 att cct ggg att gtc acc ggt ggg ctc gag ctt tgg gaa ggc aaa caa 503  
60 Ile Pro Gly Ile Val Thr Gly Gly Leu Glu Leu Trp Glu Gly Lys Gln  
61 115 120 125

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63 tgc gct gat ggt tta ttt aga aaa cgt ttg tgg ggt gga act ttt ggt      551
64 Cys Ala Asp Gly Leu Phe Arg Lys Arg Leu Trp Gly Gly Thr Phe Gly
65      130                      135                      140
67 gaa gtc tac aaa agg cct cta tgt tgg gtg gaa cac atg tca ctt gac      599
68 Glu Val Tyr Lys Arg Pro Leu Cys Trp Val Glu His Met Ser Leu Asp
69 145                      150                      155                      160
71 aat gaa act ggg ttg gat cca gct ggt att aga gtt cga gct gta tca      647
72 Asn Glu Thr Gly Leu Asp Pro Ala Gly Ile Arg Val Arg Ala Val Ser
73      165                      170                      175
75 gga ctc gtg gct gct gac tac ttt gct cct ggc tac ttt gtc tgg gca      695
76 Gly Leu Val Ala Ala Asp Tyr Phe Ala Pro Gly Tyr Phe Val Trp Ala
77      180                      185                      190
79 gtg ctg att gct aac ctt gca cat att gga tat gaa gag aaa aat atg      743
80 Val Leu Ile Ala Asn Leu Ala His Ile Gly Tyr Glu Glu Lys Asn Met
81      195                      200                      205
83 tac atg gct gca tat gac tgg cgg ctt tcg ttt cag aac aca gag gta      791
84 Tyr Met Ala Ala Tyr Asp Trp Arg Leu Ser Phe Gln Asn Thr Glu Val
85      210                      215                      220
87 cgt gat cag act ctt agc cgt atg aaa agt aat ata gag ttg atg gtt      839
88 Arg Asp Gln Thr Leu Ser Arg Met Lys Ser Asn Ile Glu Leu Met Val
89 225                      230                      235                      240
91 tct acc aac ggt gga aaa aaa gca gtt ata gtt ccg cat tcc atg ggg      887
92 Ser Thr Asn Gly Gly Lys Lys Ala Val Ile Val Pro His Ser Met Gly
93      245                      250                      255
95 gtc ttg tat ttt cta cat ttt atg aag tgg gtt gag gca cca gct cct      935
96 Val Leu Tyr Phe Leu His Phe Met Lys Trp Val Glu Ala Pro Ala Pro
97      260                      265                      270
99 ctg ggt ggc ggg ggt ggg cca gat tgg tgt gca aag tat att aag gcg      983
100 Leu Gly Gly Gly Gly Gly Pro Asp Trp Cys Ala Lys Tyr Ile Lys Ala
101      275                      280                      285
103 gtg atg aac att ggt gga cca ttt ctt ggt gtt cca aaa gct gtt gca      1031
104 Val Met Asn Ile Gly Gly Pro Phe Leu Gly Val Pro Lys Ala Val Ala
105      290                      295                      300
107 ggg ctt ttc tct gct gaa gca aag gat gtt gca gtt gcc aga gcg att      1079
108 Gly Leu Phe Ser Ala Glu Ala Lys Asp Val Ala Val Ala Arg Ala Ile
109 305                      310                      315                      320
111 gcc cca gga ttc tta gac acc gat ata ttt aga ctt cag acc ttg cag      1127
112 Ala Pro Gly Phe Leu Asp Thr Asp Ile Phe Arg Leu Gln Thr Leu Gln
113      325                      330                      335
115 cat gta atg aga atg aca cgc aca tgg gac tca aca atg tct atg tta      1175
116 His Val Met Arg Met Thr Arg Thr Trp Asp Ser Thr Met Ser Met Leu
117      340                      345                      350
119 ccg aag gga ggt gac acg ata tgg ggc ggg ctt gat tgg tca ccg gag      1223
120 Pro Lys Gly Gly Asp Thr Ile Trp Gly Gly Leu Asp Trp Ser Pro Glu
121      355                      360                      365
123 aaa ggc cac acc tgt tgt ggg aaa aag caa aag aac aac gaa act tgt      1271
124 Lys Gly His Thr Cys Cys Gly Lys Lys Gln Lys Asn Asn Glu Thr Cys
125      370                      375                      380
127 ggt gaa gca ggt gaa aac gga gtt tcc aag aaa agt cct gtt aac tat      1319

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128	Gly	Glu	Ala	Gly	Glu	Asn	Gly	Val	Ser	Lys	Lys	Ser	Pro	Val	Asn	Tyr	
129	385					390					395					400	
131	gga	agg	atg	ata	tct	ttt	ggg	aaa	gaa	gta	gca	gag	gct	gcg	cca	tct	1367
132	Gly	Arg	Met	Ile	Ser	Phe	Gly	Lys	Glu	Val	Ala	Glu	Ala	Ala	Pro	Ser	
133					405					410					415		
135	gag	att	aat	aat	att	gat	ttt	cga	ggt	gct	gtc	aaa	ggt	cag	agt	atc	1415
136	Glu	Ile	Asn	Asn	Ile	Asp	Phe	Arg	Gly	Ala	Val	Lys	Gly	Gln	Ser	Ile	
137					420					425					430		
139	cca	aat	cac	acc	tgt	cgt	gac	gtg	tgg	aca	gag	tac	cat	gac	atg	gga	1463
140	Pro	Asn	His	Thr	Cys	Arg	Asp	Val	Trp	Thr	Glu	Tyr	His	Asp	Met	Gly	
141					435				440					445			
143	att	gct	ggg	atc	aaa	gct	atc	gct	gag	tat	aag	gtc	tac	act	gct	ggt	1511
144	Ile	Ala	Gly	Ile	Lys	Ala	Ile	Ala	Glu	Tyr	Lys	Val	Tyr	Thr	Ala	Gly	
145		450				455						460					
147	gaa	gct	ata	gat	cta	cta	cat	tat	gtt	gct	cct	aag	atg	atg	gcg	cgt	1559
148	Glu	Ala	Ile	Asp	Leu	Leu	His	Tyr	Val	Ala	Pro	Lys	Met	Met	Ala	Arg	
149	465					470						475				480	
151	ggt	gcc	gct	cat	ttc	tct	tat	gga	att	gct	gat	gat	ttg	gat	gac	acc	1607
152	Gly	Ala	Ala	His	Phe	Ser	Tyr	Gly	Ile	Ala	Asp	Asp	Leu	Asp	Asp	Thr	
153					485					490					495		
155	aag	tat	caa	gat	ccc	aaa	tac	tgg	tca	aat	ccg	tta	gag	aca	aaa	tta	1655
156	Lys	Tyr	Gln	Asp	Pro	Lys	Tyr	Trp	Ser	Asn	Pro	Leu	Glu	Thr	Lys	Leu	
157					500				505					510			
159	ccg	aat	gct	cct	gag	atg	gaa	atc	tac	tca	tta	tac	gga	gtg	ggg	ata	1703
160	Pro	Asn	Ala	Pro	Glu	Met	Glu	Ile	Tyr	Ser	Leu	Tyr	Gly	Val	Gly	Ile	
161					515				520					525			
163	cca	acg	gaa	cga	gca	tac	gta	tac	aag	ctt	aac	cag	tct	ccc	gac	agt	1751
164	Pro	Thr	Glu	Arg	Ala	Tyr	Val	Tyr	Lys	Leu	Asn	Gln	Ser	Pro	Asp	Ser	
165		530					535					540					
167	tgc	atc	ccc	ttt	cag	ata	ttc	act	tct	gct	cac	gag	gag	gac	gaa	gat	1799
168	Cys	Ile	Pro	Phe	Gln	Ile	Phe	Thr	Ser	Ala	His	Glu	Glu	Asp	Glu	Asp	
169	545					550					555					560	
171	agc	tgt	ctg	aaa	gca	gga	gtt	tac	aat	gtg	gat	ggg	gat	gaa	aca	gta	1847
172	Ser	Cys	Leu	Lys	Ala	Gly	Val	Tyr	Asn	Val	Asp	Gly	Asp	Glu	Thr	Val	
173					565					570					575		
175	ccc	gtc	cta	agt	gcc	ggg	tac	atg	tgt	gca	aaa	gcg	tgg	cgt	ggc	aag	1895
176	Pro	Val	Leu	Ser	Ala	Gly	Tyr	Met	Cys	Ala	Lys	Ala	Trp	Arg	Gly	Lys	
177					580				585					590			
179	aca	aga	ttc	aac	cct	tcc	gga	atc	aag	act	tat	ata	aga	gaa	tac	aat	1943
180	Thr	Arg	Phe	Asn	Pro	Ser	Gly	Ile	Lys	Thr	Tyr	Ile	Arg	Glu	Tyr	Asn	
181					595				600					605			
183	cac	tct	ccg	ccg	gct	aac	ctg	ttg	gaa	ggg	cgc	ggg	acg	cag	agt	ggt	1991
184	His	Ser	Pro	Pro	Ala	Asn	Leu	Leu	Glu	Gly	Arg	Gly	Thr	Gln	Ser	Gly	
185					610				615					620			
187	gcc	cat	gtt	gat	atc	atg	gga	aac	ttt	gct	ttg	atc	gaa	gat	atc	atg	2039
188	Ala	His	Val	Asp	Ile	Met	Gly	Asn	Phe	Ala	Leu	Ile	Glu	Asp	Ile	Met	
189	625					630					635				640		
191	agg	gtt	gcc	gcc	gga	ggt	aac	ggg	tct	gat	ata	gga	cat	gac	cag	gtc	2087
192	Arg	Val	Ala	Ala	Gly	Gly	Asn	Gly	Ser	Asp	Ile	Gly	His	Asp	Gln	Val	

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199 atatcatgat ctctttaagc tgtcctgtca gcttatgtga atccaatact ttgaaagaga      2195
201 gatcatcatc aattcatcat catcgtcatc atcatgatgc tcaactcaca aagaagcctg      2255
203 agaatgatac tttgggtgcga aattctcaat acctctttaa tattcttatt gaatgtaaat      2315
205 tatacaatcc tatctaattgt ttgaacgata acacaaaact tgctgcgcca tgtttgtttg      2375
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212 <211> LENGTH: 671
214 <212> TYPE: PRT
216 <213> ORGANISM: Physcomitrella patens
219 <400> SEQUENCE: 2
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225          20          25          30
227 Glu Ser Ser Lys Ser His His Lys Lys Ser Asn Gly Gly Gly Lys Trp
228          35          40          45
230 Ser Cys Ile Asp Ser Cys Cys Trp Phe Ile Gly Cys Val Cys Val Thr
231          50          55          60
233 Trp Trp Phe Leu Leu Phe Leu Tyr Asn Ala Met Pro Ala Ser Phe Pro
234 65          70          75          80
236 Gln Tyr Val Thr Glu Arg Ile Thr Gly Pro Leu Pro Asp Pro Pro Gly
237          85          90          95
239 Val Lys Leu Lys Lys Glu Gly Leu Lys Ala Lys His Pro Val Val Phe
240          100          105          110
243 Ile Pro Gly Ile Val Thr Gly Gly Leu Glu Leu Trp Glu Gly Lys Gln
244          115          120          125
246 Cys Ala Asp Gly Leu Phe Arg Lys Arg Leu Trp Gly Gly Thr Phe Gly
247          130          135          140
249 Glu Val Tyr Lys Arg Pro Leu Cys Trp Val Glu His Met Ser Leu Asp
250 145          150          155          160
253 Asn Glu Thr Gly Leu Asp Pro Ala Gly Ile Arg Val Arg Ala Val Ser
254          165          170          175
256 Gly Leu Val Ala Ala Asp Tyr Phe Ala Pro Gly Tyr Phe Val Trp Ala
257          180          185          190
259 Val Leu Ile Ala Asn Leu Ala His Ile Gly Tyr Glu Glu Lys Asn Met
260          195          200          205
262 Tyr Met Ala Ala Tyr Asp Trp Arg Leu Ser Phe Gln Asn Thr Glu Val
263          210          215          220
265 Arg Asp Gln Thr Leu Ser Arg Met Lys Ser Asn Ile Glu Leu Met Val
266 225          230          235          240
268 Ser Thr Asn Gly Gly Lys Lys Ala Val Ile Val Pro His Ser Met Gly
269          245          250          255
271 Val Leu Tyr Phe Leu His Phe Met Lys Trp Val Glu Ala Pro Ala Pro
272          260          265          270
274 Leu Gly Gly Gly Gly Gly Pro Asp Trp Cys Ala Lys Tyr Ile Lys Ala

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275          275          280          285
278 Val Met Asn Ile Gly Gly Pro Phe Leu Gly Val Pro Lys Ala Val Ala
279          290          295          300
281 Gly Leu Phe Ser Ala Glu Ala Lys Asp Val Ala Val Ala Arg Ala Ile
282 305          310          315          320
284 Ala Pro Gly Phe Leu Asp Thr Asp Ile Phe Arg Leu Gln Thr Leu Gln
285          325          330          335
287 His Val Met Arg Met Thr Arg Thr Trp Asp Ser Thr Met Ser Met Leu
288          340          345          350
290 Pro Lys Gly Gly Asp Thr Ile Trp Gly Gly Leu Asp Trp Ser Pro Glu
291          355          360          365
293 Lys Gly His Thr Cys Cys Gly Lys Lys Gln Lys Asn Asn Glu Thr Cys
294          370          375          380
296 Gly Glu Ala Gly Glu Asn Gly Val Ser Lys Lys Ser Pro Val Asn Tyr
297 385          390          395          400
299 Gly Arg Met Ile Ser Phe Gly Lys Glu Val Ala Glu Ala Ala Pro Ser
300          405          410          415
302 Glu Ile Asn Asn Ile Asp Phe Arg Gly Ala Val Lys Gly Gln Ser Ile
303          420          425          430
305 Pro Asn His Thr Cys Arg Asp Val Trp Thr Glu Tyr His Asp Met Gly
306          435          440          445
308 Ile Ala Gly Ile Lys Ala Ile Ala Glu Tyr Lys Val Tyr Thr Ala Gly
309          450          455          460
311 Glu Ala Ile Asp Leu Leu His Tyr Val Ala Pro Lys Met Met Ala Arg
312 465          470          475          480
314 Gly Ala Ala His Phe Ser Tyr Gly Ile Ala Asp Asp Leu Asp Asp Thr
315          485          490          495
317 Lys Tyr Gln Asp Pro Lys Tyr Trp Ser Asn Pro Leu Glu Thr Lys Leu
318          500          505          510
320 Pro Asn Ala Pro Glu Met Glu Ile Tyr Ser Leu Tyr Gly Val Gly Ile
321          515          520          525
323 Pro Thr Glu Arg Ala Tyr Val Tyr Lys Leu Asn Gln Ser Pro Asp Ser
324          530          535          540
326 Cys Ile Pro Phe Gln Ile Phe Thr Ser Ala His Glu Glu Asp Glu Asp
327 545          550          555          560
329 Ser Cys Leu Lys Ala Gly Val Tyr Asn Val Asp Gly Asp Glu Thr Val
330          565          570          575
332 Pro Val Leu Ser Ala Gly Tyr Met Cys Ala Lys Ala Trp Arg Gly Lys
333          580          585          590
335 Thr Arg Phe Asn Pro Ser Gly Ile Lys Thr Tyr Ile Arg Glu Tyr Asn
336          595          600          605
338 His Ser Pro Pro Ala Asn Leu Leu Glu Gly Arg Gly Thr Gln Ser Gly
339          610          615          620
341 Ala His Val Asp Ile Met Gly Asn Phe Ala Leu Ile Glu Asp Ile Met
342 625          630          635          640
344 Arg Val Ala Ala Gly Gly Asn Gly Ser Asp Ile Gly His Asp Gln Val
345          645          650          655
347 His Ser Gly Ile Phe Glu Trp Ser Glu Arg Ile Asp Leu Lys Leu
348          660          665          670

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## VERIFICATION SUMMARY

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No  
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:10 M:283 W: Missing Blank Line separator, <160> field identifier  
L:12 M:283 W: Missing Blank Line separator, <210> field identifier

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